

SEQUENCE LISTING

<110> The University of Queensland (all designated States except US)  
Frazer, Ian Hector and Zhou, Jian (US only)

<120> METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL  
EFFICIENCY OF A CODON

<130> 10338-5US

<140> Not yet assigned

<141> Herewith

<150> AU PP8078

<151> 1999-01-08

<150> PCT/AU00/0008

<151> 2000-01-07

<160> 180

<170> PatentIn Ver. 2.0

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<211> 732

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Ala(GCA)5GFP

<220>

<221> CDS

<222> (1)..(732)

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Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	

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ctg ctg gag ttt gtg aoc gct gct ggg atc aca cat ggc atg gac gag 720  
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225 230 235 240

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<210> 2
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<213> Artificial Sequence
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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 3  
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45

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ctg tac aag tga  
Leu Tyr Lys 732

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<210> 4
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Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
   1                               5                10                15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                25                30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc      144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                40                45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca      192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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ctg tac aag tga  
Leu Tyr Lys

732

<210> 6  
<211> 243  
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<213> Artificial Sequence

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140  
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160  
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

1099020 5440050

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

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<220>  
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<220>  
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 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80

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<210> 8  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

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 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Lys His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205

095007460607

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
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Leu Tyr Lys

<210> 9

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<212> DNA

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<222> (1)..(732)

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Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

109920550

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150				155					160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 10  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr
Gln 210	Ser	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val
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Leu Tyr Lys

<220>  
<223> Description of Artificial Sequence: Arg(AGG)5GFP

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gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
		35					40					45					
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
	50					55					60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
65					70					75					80		
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				



acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115						120				125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130				135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
		145			150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
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ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 12  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

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 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
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<210> 13
<211> 732
<212> DNA
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<220>  
<223> Description of Artificial Sequence: Arg(CGA)5GFP

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Met	Arg	Arg	Arg	Arg	Arg	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1				5					10					15			
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
		35					40					45					
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
	50					55					60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
65					70				75						80		
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480  
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528  
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624  
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

ctg tac aag tga 732  
Leu Tyr Lys

<210> 14  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<400> 14  
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

179020-5400550

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 15  
<211> 732  
<212> DNA



Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

50		55		60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro				
65		70		75
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly				
	85		90	95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys				
	100		105	110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile				
	115		120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His				
	130		135	140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp				
	145		150	155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile				
	165		170	175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro				
	180		185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr				
	195		200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val				
	210		215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu				
	225		230	235
				240
Leu Tyr Lys				

<210> 17  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Arg(CGG)5GFP



<222> (1) .. (732)

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160



Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
Leu	Tyr	Lys														

<210> 19  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Arg(CGT)5GFP  
  
 <220>  
 <221> CDS  
 <222> (1)..(732)

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<400>	20															
Met	Arg	Arg	Arg	Arg	Arg	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 21  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Asn(AAC)5GFP

<220>  
<221> CDS  
<222> (1)..(732)

<400> 21  
atg aac aac aac aac aac agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

1				5				10				15				
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
20				25				30								
tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
35				40				45								
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
50				55				60								
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65				70				75				80				
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
85				90				95								
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
100				105				110								
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
115				120				125								
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
130				135				140								
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145				150				155				160				
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
165				170				175								
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
180				185				190								

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624  
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

ctg tac aag tga 732  
Leu Tyr Lys

<210> 22  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<400> 22  
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile



115	120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140		
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160		
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175		
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190		
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205		
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220		
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240		
Leu Tyr Lys		

<210> 23  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Asn(AAT)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 23	
atg aat aat aat aat aat agc aag ggc gag gaa ctg ttc act ggc gtg 48	
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96	
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	





Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 25  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Asp(GAC)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 25  
 atg gac gac gac gac gac agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

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ctg tac aag tga 732  
Leu Tyr Lys

<400>	26															
Met	Asp	Asp	Asp	Asp	Asp	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145				150						155					160	

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<210> 27
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asp(GAT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 27
atg gat gat gat gat gat agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
   1                               5                               10                               15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                               20                               25                               30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc      144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
           35                               40                               45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca      192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

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50	55	60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca			240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
65	70	75	80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc			288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
	85	90	95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag			336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
	100	105	110
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc			384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
	115	120	125
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac			432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
	130	135	140
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
	145	150	155
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235
			240

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<400>	28															
Met	Asp	Asp	Asp	Asp	Asp	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	

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<210> 29
<211> 732
<212> DNA
<213> Artificial Sequence
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<220>
<221> CDS
<222> (1)..(732)
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-xlii-

-xliii-

<210> 30  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 30  
 Met Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205

105020 070601

<400>	31																	
atg	tgt	tgt	tgt	tgt	tgt	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48		
Met	Cys	Cys	Cys	Cys	Cys	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val			
1				5					10					15				
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe			
			20					25					30					
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr			
		35					40					45						
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192		
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr			
	50					55					60							
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240		
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro			
65					70					75					80			
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288		
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly			

	85	90	95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag				336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	100	105	110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc				384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	115	120	125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac				432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	130	135	140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac				480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	145	150	155	160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att				528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	165	170	175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca				576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc				624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc				672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag				720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	225	230	235	240
ctg tac aag tga				732
Leu Tyr Lys				

<210> 32  
 <211> 243  
 <212> PRT

<400> 32

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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 33  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Gln(CAA)5GFP

<220>  
<221> CDS  
<222> (1)..(732)

<400> 33  
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gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca 192  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95  
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys



100										105					110					
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384				
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile					
115						120			125											
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His					
130						135			140											
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp					
145			150			155			160											
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528				
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile					
			165						170			175								
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576				
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro					
180						185			190											
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624				
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr					
195						200			205											
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672				
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val					
210			215			220														
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu					
225			230			235			240											
ctg	tac	aag	tga												732					
Leu	Tyr	Lys																		

<210> 34  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 34  
 Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

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Ser Val Ser 35	Gly Glu Gly Glu Gly 40	Asp Ala Thr Tyr Gly 45	Lys Leu Thr
Leu Lys Phe Ile Cys Thr Thr 50	Gly Lys Leu Pro Val Pro Trp Pro Thr 55		
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65		75	80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85		90	95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100		105	110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115		120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130		135	140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145		150	155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165		170	175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180		185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195		200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210		215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225		230	235
Leu Tyr Lys			240

protein data bank

<210> 35  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gln(CAG)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

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 1 5 10 15  
 gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile

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115	120	125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac			432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
130	135	140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
145	150	155	160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
165	170	175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
195	200	205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
225	230	235	240
ctg tac aag tga			732
Leu Tyr Lys			
<210> 36			
<211> 243			
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
20	25	30	

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 37  
<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 37

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	

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130	135	140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac			480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
145	150	155	160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att			528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
	165	170	175
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca			576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
	180	185	190
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
	195	200	205
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
	210	215	220
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
	225	230	235
ctg tac aag tga			732
Leu Tyr Lys			
<210> 38			
<211> 243			
<212> PRT			
<213> Artificial Sequence			
<400> 38			
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val			
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe			
	20	25	30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr			
	35	40	45

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<210> 39
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
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<223> Description of Artificial Sequence: Glu(GAG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 39

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Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	

090034-07004

145	150								155								160								
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528									
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile										
				165					170					175											
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576									
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro										
			180					185					190												
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624									
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr										
		195					200					205													
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672									
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val										
	210					215					220														
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720									
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu										
225					230					235					240										
ctg	tac	aag	tga													732									
Leu	Tyr	Lys																							
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Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe										
			20					25					30												
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr										
		35					40					45													
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr										
	50					55					60														
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro										

65		70		75		80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly						
	85			90		95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys						
	100			105		110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile						
	115			120		125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His						
	130			135		140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp						
	145			150		155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile						
	165			170		175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro						
	180			185		190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr						
	195			200		205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val						
	210			215		220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu						
	225			230		235
						240

Leu Tyr Lys

<210> 41  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gly(GGA)5GFP

<220>  
 <221> CDS

<400> 41

-1x-

-lxi-

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		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
		130				135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
		145			150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
		210				215					220					
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
		225			230					235					240	
Leu	Tyr	Lys														

<210> 43  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gly(GGC)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 43  
 atg ggc ggc ggc ggc ggc agc aag ggc gag gaa ctg ttc act ggc gtg 48

Met 1	Gly	Gly	Gly	Gly 5	Gly	Ser	Lys	Gly	Glu 10	Glu	Leu	Phe	Thr	Gly 15	Val	
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55				60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130				135						140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	

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180	185	190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc			624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
195	200	205	
cag tct gcc ctg tot aaa gat ccc aac gaa aag aga gac cac atg gtc			672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
210	215	220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag			720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu			
225	230	235	240
ctg tac aag tga			732
Leu Tyr Lys			

<210> 44  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 44  
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110



Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 45  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gly(GGG)5GFP  
 <220>  
 <221> CDS  
 <222> (1)..(732)

<400> 45  
 atg ggg ggg ggg ggg ggg agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96

Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggg Gly	gaa Glu	ggg Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly 110	aac Asn	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggg Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu	cca Pro	gac Asp	aac Asn	cat His	tac Tyr	ctg Leu	tcc Ser	acc Thr	624

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<210> 46
<211> 243
<212> PRT
<213> Artificial Sequence
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-lxvii-

130		135		140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp				
145		150		155 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile				
	165		170	175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro				
	180		185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr				
	195		200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val				
	210		215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu				
225		230		235 240

Leu Tyr Lys

<210> 47  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gly(GGT)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 47  
 atg ggt ggt ggt ggt ggt agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Gly Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144



ctg tac aag tga  
Leu Tyr Lys 732

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<400> 48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1          5          10          15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
          20          25          30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35          40          45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50          55          60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65          70          75          80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
          85          90          95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
          100          105          110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
          115          120          125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130          135          140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
    145          150          155          160

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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190  
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220  
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240  
Leu Tyr Lys

<210> 49  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: His(CAC)5GFP

<220>  
<221> CDS  
<222> (1)..(732)

<400> 49  
atg cac cac cac cac cac agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15  
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192





732

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<210> 50
<211> 243
<212> PRT
<213> Artificial Sequence
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<400> 50

Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145                      150                      155                      160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

<400> 51																	
atg	cat	cat	cat	cat	cat	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48	
Met	His	His	His	His	His	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1					5				10					15			
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				
tct	gtc	agc	gga	gag	ggc	gaa	ggc	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
		35					40					45					
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
	50					55					60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	

-1xxv-

<210> 52  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 52  
 Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr

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195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 53  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ile(ATA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 53  
 atg ata ata ata ata ata agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288

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Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
			115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
			130				135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
						150				155					160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
						165				170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
						180								190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
								200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
							215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
						230				235					240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

<210> 54  
<211> 243

<213> Artificial Sequence

Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Tyr Lys

<220>  
<223> Description of Artificial Sequence: Ile(ATC)5GFP

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<220>
<221> CDS
<222> (1)..(732)
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gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95



Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
		130				135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
145					150					155					160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165						170					175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
		195					200					205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
		210				215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
225					230				235						240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

<210> 56  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence  
 <400> 56

Met	Ile	Ile	Ile	Ile	Ile	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	1	5	10	15
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	20	25	30	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	35	40	45	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	50	55	60	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	65	70	75	80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	85	90	95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	100	105	110	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	115	120	125	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	130	135	140	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	145	150	155	160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	165	170	175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	180	185	190	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	195	200	205	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	210	215	220	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	225	230	235	240

Leu Tyr Lys

<210> 57  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ile(ATT)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 57  
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 Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384

690643.0001

Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
	130					135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
	145				150					155					160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165						170					175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
		195					200					205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
	210					215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
	225				230				235						240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															
 <210> 58																	
<211> 243																	
<212> PRT																	
<213> Artificial Sequence																	
 <400> 58																	
Met	Ile	Ile	Ile	Ile	Ile	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1				5					10					15			
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe																	

<210> 59

<400>	59															
atg	cta	cta	cta	cta	cta	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432

Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
130						135					140						
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
145				150						155				160			
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165					170					175				
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
		195				200						205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
		210				215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
225				230				235						240			
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															

<210> 60  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 60  
 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 61  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence



<223> Description of Artificial Sequence: Leu(CTC)5GFP

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (732)$ 

atg	ctc	ctc	ctc	ctc	ctc	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
tct	gtc	agc	gga	gag	ggg	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120				125					
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480

Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														
<210> 62																
<211> 243																
<212> PRT																
<213> Artificial Sequence																
<400> 62																
Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					

Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
			85						90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
		100						105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145				150						155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
			165						170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
	195						200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240

Leu Tyr Lys

<210> 63

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTG)5GFP

<220>

$\langle 222 \rangle \quad (1) \dots (732)$ 

atg Met 1	ctg Leu	ctg Leu	ctg Leu	ctg Leu 5	ctg Leu	agc Ser	aag Lys	ggc Gly	gag Glu 10	gaa Glu	ctg Leu	ttc Phe	act Thr	ggc Gly 15	gtg Val	48
gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggg Gly	gaa Glu	ggg Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly 110	aac Asn	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggg Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu 130	ctg Leu	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly 140	aac Asn	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn 150	tat Tyr	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528

Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
				165					170					175			
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
			195				200					205					
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
	210					215					220						
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
	225				230					235					240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															
<210> 64																	
<211> 243																	
<212> PRT																	
<213> Artificial Sequence																	
<400> 64																	
Met	Leu	Leu	Leu	Leu	Leu	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1				5				10						15			
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
			35				40					45					
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
	50					55					60						
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
	65				70					75					80		
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		

				85						90					95			
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys			
			100					105					110					
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile			
		115					120					125						
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His			
	130					135					140							
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp			
145					150					155					160			
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile			
			165						170					175				
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro			
			180					185					190					
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr			
		195					200					205						
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val			
	210					215					220							
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu			
225					230					235					240			

Leu Tyr Lys

<210> 65

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 65

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<210> 66
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 66
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1                               5                10                15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                25                30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35                40                45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50                55                60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                70                75                80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                90                95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
          100                105                110

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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 67  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Leu(TTA)5GFP

<220>  
<221> CDS  
<222> (1)..(732)

<400> 67  
atg tta tta tta tta tta agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

-xcviii-

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<210> 68
<211> 243
<212> PRT
<213> Artificial Sequence
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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 69  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Leu(TTG)5GFP

<220>  
<221> CDS  
<222> (1)..(732)

<400> 69  
atg ttg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672

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<210> 70
<211> 243
<212> PRT
<213> Artificial Sequence
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145		150		155		160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile						
		165		170		175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro						
		180		185		190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr						
		195		200		205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val						
		210		215		220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu						
		225		230		235
						240

Leu Tyr Lys

<210> 71  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Lys(AAA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 71

atg aaa aaa aaa aaa aaa agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	

-civ-



732

<400>	72															
Met	Lys	Lys	Lys	Lys	Lys	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 73  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Lys(AAG)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 73  
 atg aag aag aag aag aag agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732

Leu Tyr Lys

<210> 74  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<400> 74  
Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140  
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160  
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

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<400>	75																
atg	ttt	ttt	ttt	ttt	ttt	agg	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48	
Met	Phe	Phe	Phe	Phe	Phe	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1				5					10					15			
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				
tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
		35					40					45					
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
	50					55					60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
65					70				75						80		

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 76

<211> 243  
<212> PRT  
<213> Artificial Sequence

<400> 76

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Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1           5           10           15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
      20           25           30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
      35           40           45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50           55           60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65           70           75           80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
      85           90           95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
      100          105          110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
      115          120          125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130          135          140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145          150          155          160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
      165          170          175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
      180          185          190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195          200          205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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650045-07004

210	215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
225	230	235 240

Leu Tyr Lys

<210> 77  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Phe(TTC)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 77

atg ttc ttc ttc ttc ttc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	

109020640660



tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
		100						105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130					135					140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230					235					240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 78

<211> 243

<212> PRT

<213> Artificial Sequence

-cxiv-

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<220>
<223> Description of Artificial Sequence: Pro(CCC)5GFP
<220>
<221> CDS
<222> (1)..(732)
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- CXV -

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	
<210> 80	
<211> 243	
<212> PRT	
<213> Artificial Sequence	
<400> 80	
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	



<400>	81																
atg	ccg	ccg	ccg	ccg	ccg	agg	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48	
Met	Pro	Pro	Pro	Pro	Pro	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1					5				10					15			
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
			20					25					30				
tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
		35					40					45					
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
	50					55					60						
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
65					70					75					80		
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggg	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480  
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528  
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624  
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

ctg tac aag tga 732  
Leu Tyr Lys

<210> 82  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<400> 82  
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

105020405060

35	40	45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr		
50	55	60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro		
65	70	75
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly		
	85	90
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys		
	100	105
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile		
	115	120
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His		
	130	135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp		
	145	150
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile		
	165	170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro		
	180	185
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		
	195	200
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
	210	215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
	225	230
		235
		240
Leu Tyr Lys		

<210> 83  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence



<223> Description of Artificial Sequence: Pro(CCT)5GFP

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (732)$ 

atg Met 1	cct Pro	cct Pro	cct Pro	cct Pro 5	cct Pro	agc Ser	aag Lys	ggc Gly	gag Glu 10	gaa Glu	ctg Leu	ttc Phe	act Thr	ggc Gly 15	gtg Val	48
gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly 30	cac His	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggg Gly	gaa Glu	ggg Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr 45	gga Gly	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln 100	gag Glu	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly 110	aac Asn	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggg Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly 140	aac Asn	att Ile	ctc Leu	ggc Gly	cac His	432

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aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                      150                      155                      160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                      170                      175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                      185                      190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                      200                      205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210                      215                      220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                      230                      235                      240

ctg tac aag tga
Leu Tyr Lys 732

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<210> 84
<211> 243
<212> PRT
<213> Artificial Sequence

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<400> 84
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1                      5                      10                      15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                25                30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35                40                45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 50                55                60

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Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
	195						200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu
225					230					235					240
Leu	Tyr	Lys													

<210> 85  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Pro(CGA)5GFP

$\langle 222 \rangle \quad (1) \dots (732)$ 

atg cga cga cga cga cga agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480  
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
                   165                  170                  175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
                   180                  185                  190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
                   195                  200                  205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
                   210                  215                  220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
                   225                  230                  235                  240

ctg tac aag tga 732  
 Leu Tyr Lys

<210> 86  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 86  
 Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
   1                  5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
                   20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
                   35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
                   50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
                   65                  70                  75                  80

Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
		100						105					110				
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
		115					120					125					
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
	130					135					140						
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
145				150					155						160		
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
			165						170					175			
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185					190				
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
		195					200					205					
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
	210					215					220						
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
225					230					235					240		

Leu Tyr Lys

<210> 87

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(AGC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 87

atg agc agc agc agc agc agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctg gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctg acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctg cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctg ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 88  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 88  
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys



100	105	110
Thr Arg Ala Glu Val Lys Phe	Glu Gly Asp Thr Leu Val Asn Arg Ile	
115	120	125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His		
130	135	140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp		
145	150	155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile		
165	170	175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro		
180	185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		
195	200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
210	215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
225	230	235
		240

Leu Tyr Lys

<210> 89  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(AGT)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 89  
 atg agt agt agt agt agt agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 90  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 90
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 91  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(TCA)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 91  
 atg tca tca tca tca tca agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

ctg tac aag tga 732  
Leu Tyr Lys

<210> 92  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<400> 92  
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

09500046-07603

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

Leu Tyr Lys

<210> 93  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(TCC)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 93  
 atg tcc tcc tcc tcc tcc agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45

09907054060

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
	65				70					75					80	
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	
				85					90					95		
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	
			100					105					110			
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggc	gac	acc	ctg	gtg	aac	aga	atc	384
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	
		115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
	130				135						140					
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aac	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
	145				150					155					160	
aag	caa	aag	aac	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					



ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240

ctg tac aag tga 732  
 Leu Tyr Lys

<210> 94  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 94  
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80  
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 85 90 95  
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 100 105 110  
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 115 120 125  
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 130 135 140  
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile

0900345-070604

	165		170		175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	180	185	190		
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	195	200	205		
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	210	215	220		
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	225	230	235	240	
Leu Tyr Lys					

<210> 95  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(TCG)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 95  
 atg tcg tcg tcg tcg tcg agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ser Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60

-CXXXIX-

732

<400>	96														
Met	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145				150						155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 97  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Ser(TCT)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 97  
 atg tct tct tct tct tct agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 35 40 45  
 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 50 55 60  
 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
 65 70 75 80



<210> 98  
<211> 243  
<212> PRT  
<213> Artificial Sequence

<400> 98  
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95  
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110  
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125  
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140  
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160  
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190  
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

099020540560

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 99  
<211> 732  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Thr(ACA)5GFP

<220>  
<221> CDS  
<222> (1)..(732)

<400> 99  
atg aca aca aca aca aca agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
1 5 10 15  
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
20 25 30  
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45  
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192  
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60  
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240  
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80  
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288  
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Truncated



tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 100

<211> 243

<212> PRT

<213> Artificial Sequence

Met	Thr	Thr	Thr	Thr	Thr	Ser	Lys	Gly	Glu	Leu	Phe	Thr	Gly	Val	
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Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
	65				70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
	145				150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val
	210					215					220				
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu

240

<400> 101																	
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Met	Thr	Thr	Thr	Thr	Thr	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val		
1				5				10				15					
gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe		
				20				25				30					
tct	gtc	agc	gga	gag	ggt	gaa	ggt	gat	gcc	aca	tac	gga	aag	ctc	acc	144	
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr		
35								40				45					
ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192	
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr		
50								55				60					
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240	
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro		
65				70				75				80					
gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288	
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85				90				95					
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
100								105				110					

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145 150 155 160	
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
225 230 235 240	
ctg tac aag tga	732
Leu Tyr Lys	

<210> 102  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 102  
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[illegible]

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<220>
<221> CDS
<222> (1)..(732)
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Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	
130						135					140					

aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	
145					150					155					160	

aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
				165					170					175		

gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185						190		

atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				

cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					

ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	

ctg	tac	aag	tga													732
Leu	Tyr	Lys														

<210> 104  
 <211> 243  
 <212> PRT  
 <213> Artificial Sequence

<400> 104  
 Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
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 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 105  
<211> 732  
<212> DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACT)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 105

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130 135 140	

109020-070601



50		55		60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro					
65		70		75	80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly					
	85		90		95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys					
	100		105		110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile					
	115		120		125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His					
	130		135		140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp					
	145		150		155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile					
	165		170		175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro					
	180		185		190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr					
	195		200		205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val					
	210		215		220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu					
	225		230		235
					240
Leu Tyr Lys					

<210> 107

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trp(TGG)5GFP

$\langle 222 \rangle \quad (1) \dots (732)$ 

-clvi-

aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	
			165						170					175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	
			180					185					190			
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	
		195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	
	210					215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	
225					230				235						240	
ctg	tac	aag	tga													732
Leu	Tyr	Lys														
<210> 108																
<211> 243																
<212> PRT																
<213> Artificial Sequence																
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Met	Trp	Trp	Trp	Trp	Trp	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55					60					
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70					75					80	

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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
      85                      90                      95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
      100                    105                    110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
      115                    120                    125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130                    135                    140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                    150                    155                    160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
      165                    170                    175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
      180                    185                    190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
      195                    200                    205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
      210                    215                    220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                    230                    235                    240
Leu Tyr Lys

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<210> 109

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAT)5GFP

<220>

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<222> (1)..(732)

atg Met 1	tat Tyr	tat Tyr	tat Tyr	tat Tyr 5	tat Tyr	agc Ser	aag Lys	ggc Gly	gag Glu 10	gaa Glu	ctg Leu	ttc Phe	act Thr	ggc Gly 15	gtg Val	48
gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggg Gly	gaa Glu	ggg Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln 100	gag Glu	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggg Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn 150	tat Tyr	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala 160	gac Asp	480
aag Lys	caa Gln	aag Lys	aat Asn 165	ggc Gly	atc Ile	aag Lys	gtc Val	aac Asn 170	ttc Phe 175	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576  
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624  
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672  
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720  
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

ctg tac aag tga 732  
Leu Tyr Lys

<210> 110  
<211> 243  
<212> PRT  
<213> Artificial Sequence

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Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
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20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro  
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
85 90 95



Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 111

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 111

atg tac tac tac tac tac agc aag ggc gag gaa ctg ttc act ggc gtg 48  
Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

-clxii-



115		120		125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His				
130		135		140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp				
145		150		155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile				
	165		170	175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro				
	180		185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr				
	195		200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val				
	210		215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu				
225		230		235
				240
Leu Tyr Lys				

<210> 113

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 113

atg gta gta gta gta gta agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	

-clxv-



Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 145 150 155 160  
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 165 170 175  
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 180 185 190  
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr  
 195 200 205  
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 210 215 220  
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
 225 230 235 240  
 Leu Tyr Lys

<210> 115  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Val(GTC)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 115  
 atg gtc gtc gtc gtc gtc agc aag ggc gag gaa ctg ttc act ggc gtg 48  
 Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 1 5 10 15  
 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96  
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 20 25 30  
 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144  
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

35	40	45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192		
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr			
50 55 60			
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240		
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro			
65 70 75 80			
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288		
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly			
85 90 95			
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336		
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys			
100 105 110			
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384		
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile			
115 120 125			
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432		
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His			
130 135 140			
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480		
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp			
145 150 155 160			
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528		
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile			
165 170 175			
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576		
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro			
180 185 190			
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624		
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr			
195 200 205			
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672		
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val			
210 215 220			





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<210> 117
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 117
atg gtg gtg gtg gtg gtg agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Val Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
   1                               5                               10                               15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                               20                               25                               30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc      144
Ser Val Ser Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                               35                               40                               45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca      192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

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-clxxi-

732

<400>	118														
Met	Val	Val	Val	Val	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro

180	185	190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr		
195	200	205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val		
210	215	220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu		
225	230	235
		240
Leu Tyr Lys		

<210> 119  
 <211> 732  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Val(GTT)5GFP

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 119	
atg gtt gtt gtt gtt gtt agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	



<400>	120														
Met	Val	Val	Val	Val	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5					10					15	
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe
			20					25					30		
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr
		35					40					45			
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr
	50					55					60				
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro
65					70					75					80
Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly
				85					90					95	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys
			100					105					110		
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile
		115					120					125			
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His
	130					135					140				
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp
145					150					155					160
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile
				165					170					175	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro
			180					185					190		
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr
		195					200					205			

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu  
225 230 235 240

Leu Tyr Lys

<210> 121

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Stop(TAA)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 121

atg	taa	taa	taa	taa	taa	agc	aag	ggc	gag	gaa	ctg	ttc	act	ggc	gtg	48
Met						Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	
1				5					10					15		

gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96
Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	
			20					25					30			

tct	gtc	agc	gga	gag	ggg	gaa	ggg	gat	gcc	aca	tac	gga	aag	ctc	acc	144
Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	
		35					40					45				

ctg	aaa	ttc	atc	tgc	acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	192
Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	
	50					55				60						

ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240
Leu	Val	Thr	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	
65					70				75						80	

gac	cat	atg	aag	cag	cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	288
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly		
				85					90					95			
tat	gtg	cag	gag	aga	acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	336	
Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys		
			100					105					110				
acc	cgc	gct	gaa	gtc	aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	384	
Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile		
			115					120					125				
gag	ctg	aag	ggc	att	gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	432	
Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His		
			130					135					140				
aag	ctg	gaa	tac	aac	tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	480	
Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp		
						150									160		
aag	caa	aag	aat	ggc	atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	528	
Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile		
				165											175		
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	576	
Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro		
			180					185							190		
atc	ggc	gac	ggc	cct	gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	624	
Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr		
			195					200					205				
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	672	
Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val		
			210				215					220					
ctg	ctg	gag	ttt	gtg	acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	720	
Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu		
						230				235					240		
ctg	tac	aag	tga													732	
Leu	Tyr	Lys															
<210> 122																	
<211> 732																	

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Stop(TAG)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 122

atg tag tag tag tag tag agc aag ggc gag gaa ctg ttc act ggc gtg	48
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
1 5 10 15	
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt	96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
20 25 30	
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc	144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
35 40 45	
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca	192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
50 55 60	
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca	240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	
65 70 75 80	
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc	288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly	
85 90 95	
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag	336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys	
100 105 110	
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc	384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	
115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac	432

0990345-07004

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His	
130	135 140
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac	480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
145	150 155 160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att	528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	
	165 170 175
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca	576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro	
	180 185 190
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc	624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr	
	195 200 205
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc	672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val	
	210 215 220
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag	720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu	
	225 230 235 240
ctg tac aag tga	732
Leu Tyr Lys	
<210> 123	
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<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Stop(TGA)5GFP	
<220>	
<221> CDS	
<222> (1)..(732)	
<400> 123	

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atg Met 1	tga	tga	tga	tga	tga	agc Ser	aag Lys	ggc Gly	gag Glu	gaa Glu	ctg Leu	ttc Phe	act Thr	ggc Gly	gtg Val	48
51015																
gtc Val	cca Pro	att Ile	ctc Leu	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly	gat Asp	gtg Val	aat Asn	ggg Gly	cac His	aaa Lys	ttt Phe	96
20																
tct Ser	gtc Val	agc Ser	gga Gly	gag Glu	ggg Gly	gaa Glu	ggg Gly	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly	aag Lys	ctc Leu	acc Thr	144
3540																
ctg Leu	aaa Lys	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val	cca Pro	tgg Trp	cca Pro	aca Thr	192
5055																
ctg Leu	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro	240
657080																
gac Asp	cat His	atg Met	aag Lys	cag Gln	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu	ggc Gly	288
859095																
tat Tyr	gtg Val	cag Gln	gag Glu	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn	tac Tyr	aag Lys	336
100105110																
acc Thr	cgc Arg	gct Ala	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu	ggg Gly	gac Asp	acc Thr	ctg Leu	gtg Val	aat Asn	aga Arg	atc Ile	384
115120125																
gag Glu	ctg Leu	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn	att Ile	ctc Leu	ggc Gly	cac His	432
130135140																
aag Lys	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr	aac Asn	tcc Ser	cac His	aat Asn	gtg Val	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp	480
145150155160																
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe	aag Lys	atc Ile	aga Arg	cac His	aac Asn	att Ile	528
165170175																
gag	gat	gga	tcc	gtg	cag	ctg	gcc	gac	cat	tat	caa	caq	aac	act	cca	576

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acc	act	gga	aag	ctc	cct	gtg	cca	tgg	cca	aca	ctg	gtc	act	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					
tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	gac	cat	atg	aag	cag	240
Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
	65				70					75					80	
cat	gac	ttt	ttc	aag	agc	gcc	atg	ccc	gag	ggc	tat	gtg	cag	gag	aga	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		
acc	atc	ttt	ttc	aaa	gat	gac	ggg	aac	tac	aag	acc	cgc	gct	gaa	gtc	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			
aag	ttc	gaa	ggt	gac	acc	ctg	gtg	aat	aga	atc	gag	ctg	aag	ggc	att	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				
gac	ttt	aag	gag	gat	gga	aac	att	ctc	ggc	cac	aag	ctg	gaa	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130				135					140					
tat	aac	tcc	cac	aat	gtg	tac	atc	atg	gcc	gac	aag	caa	aag	aat	ggc	480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
	145				150					155					160	
atc	aag	gtc	aac	ttc	aag	atc	aga	cac	aac	att	gag	gat	gga	tcc	gtg	528
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
				165					170					175		
cag	ctg	gcc	gac	cat	tat	caa	cag	aac	act	cca	atc	ggc	gac	ggc	cct	576
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	
			180					185					190			
gtg	ctc	ctc	cca	gac	aac	cat	tac	ctg	tcc	acc	cag	tct	gcc	ctg	tct	624
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	
			195				200					205				
aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc	ctg	ctg	gag	ttt	gtg	672
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	
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acc	gct	gct	ggg	atc	aca	cat	ggc	atg	gac	gag	ctg	tac	aag	tga		717







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primer

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primer

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primer

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primer

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primer

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primer

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primer

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primer

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primer

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primer

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